

SEQUENCE LISTING

<110> LINDNER, Volkhard
FRIESEL, Robert E.

<120> COMPOSITIONS, METHODS AND KITS RELATING TO REMODELIN

<130> 053689-5006-01

<150> US 09/692,081
<151> 2000-10-19

<160> 9

<170> PatentIn version 3.1

<210> 1
<211> 1192
<212> DNA
<213> Rattus sp.

<400> 1
atgcggccgg ccgcagagct gggccagacg ctgagcaggg ccgggctctg ccgacccctt 6
0
tgctctctgc tctgcgttc gcagctaccg cacacgatgc accccaagg ccgcgcgcc 12
0
tccccacagc tgctgctcgg cctcttcctt gtgctactgc tgcttctgca gctgtccgcg 18
0
ccgtccagcg cctctgagaa tccaaggtg aagcaaaaag cgctgatccg gcagagggaa 24
0
gtggtagacc tgtataatgg gatgtgccta caaggaccag caggagttcc tggtcgcgat 30
0
gggagccctg gggccaatgg cattcctggc acaccgggaa tcccaggtcg ggatggattc 36
0
aaaggagaga aaggggagtg cttaagggaag agctttgagg aatcctggac cccaaactac 42
0
aagcagtgtt catggagttc acttaattat ggcatagatc ttgggaaaat tgcggaatgt 48
0
acattcacia agatgcgac caacagcgt cttcgagttc tggtcagtgg ctgcgttcgg 54
0
ctcaaatgca ggaatgcttg ctgtcaacgc tggatttta cctttaatgg agctgaatgt 60
0
tcaggacctc tccccattga agctatcatc tatctggacc aaggaagccc tgagttaaatt 66
0
tcaactatta atattcatcg tacttctcctc gtggaaggac tctgtgaagg gattggtgct 72
0
ggactggtag acgtggccat ctgggtcggc acctgttcag attaccccaa aggagacgct 78
0
tctactgggt ggaattctgt gtcccgcatc atcattgaag aactaccaa ataaagcccc 84
0
tgaaggtttc attccctgcc tcatttactt gttaaataca gcctctggat gggtcattta 90
0
aatgacattt cagaagtcac ttatgtgctc agccaaatga aaaagcaaag ttaaatacgt 96

```

0
ttacagacca aagtgtgac tcacacttta agatctagca ttatccattt tatttcaacc 102
0
aaagatgggtt tcaggatttt atttctcatt gattactttt tgagcctata taccggaatg 108
0
ctgttatagt ctttaatat ttctactgtt gacattttga aacatataaa agttatgtct 114
0
ttgtaagagc tgtatagaat tattttatat gttaaataaa tgcttcaaac aa 119
2

```

```

<210> 2
<211> 245
<212> PRT
<213> Rattus sp.

```

```

<400> 2

```

```

Met His Pro Gln Gly Arg Ala Ala Ser Pro Gln Leu Leu Leu Gly Leu
1          5          10          15
Phe Leu Val Leu Leu Leu Leu Leu Gln Leu Ser Ala Pro Ser Ser Ala
20          25          30
Ser Glu Asn Pro Lys Val Lys Gln Lys Ala Leu Ile Arg Gln Arg Glu
35          40          45
Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val
50          55          60
Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro
65          70          75          80
Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu
85          90          95
Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser
100         105         110
Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys
115         120         125
Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser
130         135         140
Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr
145         150         155         160
Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala
165         170         175
Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Leu Asn Ser Thr Ile Asn
180         185         190

```

Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala
195 200 205

Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro
210 215 220

Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile
225 230 235 240

Glu Glu Leu Pro Lys
245

<210> 3
<211> 1220
<212> DNA
<213> Homo sapiens

<400> 3
acgagggcgg cctcggagcg cggcggagcc agacgctgac cacgttcctc tcctcgggtct 6
0
cctccgcctc cagctccgcg ctgcccgga gccgggagcc atgcgacccc agggccccgc 12
0
cgctccccg cagcggctcc gggcctcct gctgctcctg ctgctgcagc tgcccgcgcc 18
0
gtcgagcgcc tctgagatcc ccaaggggaa gcaaaaggcg cagctccggc agagggaggt 24
0
ggtggacctg tataatggaa tgtgcttaca agggccagca ggagtgcctg gtcgagacgg 30
0
gagccctggg gccaatggca ttccgggtac acctgggatc ccaggtcggg atggattcaa 36
0
aggagaaaag ggggaatgtc tgagggaaag ctttgaggag tcctggacac ccaactacaa 42
0
gcagtgttca tggagtccat tgaattatgg catagatctt gggaaaattg cggagtgtac 48
0
atttacaag atgcgttcaa atagtgtctt aagagttttg ttcagtggct cacttcggct 54
0
aaaatgcaga aatgcatgct gtcagcgttg gtatttcaca ttcaatggag ctgaatgttc 60
0
aggacctctt ccattgaag ctataattta ttggaccaa ggaagccctg aaatgaattc 66
0
aacaattaat attcatcgca cttcttctgt ggaaggactt tgtgaaggaa ttggtgctgg 72
0
attagtggat gttgctatct gggttggcac ttgttcagat taccctaaaag gagatgcttc 78
0
tactggatgg aattcagttt ctgcgcatcat tattgaagaa ctacccaaaat aaatgcttta 84
0
attttcattt gctacctctt tttttattat gccttggaat ggttcactta aatgacattt 90
0
taaataagtt tatgtatata tctgaatgaa aagcaaagct aaatatgttt acagacccaaa 96
0
gtgtgatttc aactgtttt taaatctagc attattcatt ttgcttcaat caaaagtgggt 102

0
 ttcaatattt ttttagttgg ttagaatact ttcttcatag tcacattctc tcaacctata 108
 0
 atttggaata ttgttgtggt cttttgtttt ttctottagt atagcatttt taaaaaata 114
 0
 taaaagctac caatctttgt acaatttgta aatgttaaga atttttttta tatctgttaa 120
 0
 ataaaaatta tttccaacaa 122
 0

<210> 4
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
 20 25 30
 Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
 35 40 45
 Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
 50 55 60
 Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
 65 70 75 80
 Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
 85 90 95
 Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
 100 105 110
 Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
 115 120 125
 Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
 130 135 140
 Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
 145 150 155 160
 Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
 165 170 175
 Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
 180 185 190

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
195 200 205

Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
210 215 220

Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
225 230 235 240

Leu Pro Lys

<210> 5

<211> 277

<212> PRT

<213> Rattus sp.

<400> 5

Met Arg Pro Ala Ala Glu Leu Gly Gln Thr Leu Ser Arg Ala Gly Leu
1 5 10 15

Cys Arg Pro Leu Cys Leu Leu Leu Cys Ala Ser Gln Leu Pro His Thr
20 25 30

Met His Pro Gln Gly Arg Ala Ala Ser Pro Gln Leu Leu Leu Gly Leu
35 40 45

Phe Leu Val Leu Leu Leu Leu Leu Gln Leu Ser Ala Pro Ser Ser Ala
50 55 60

Ser Glu Asn Pro Lys Val Lys Gln Lys Ala Leu Ile Arg Gln Arg Glu
65 70 75 80

Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val
85 90 95

Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro
100 105 110

Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu
115 120 125

Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser
130 135 140

Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys
145 150 155 160

Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser
165 170 175

Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr
 180 185 190

Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala
 195 200 205

Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Leu Asn Ser Thr Ile Asn
 210 215 220

Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala
 225 230 235 240

Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro
 245 250 255

Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile
 260 265 270

Glu Glu Leu Pro Lys
 275

<210> 6
 <211> 403
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:REMODELIN antisense ribonucle
 oprobe

<400> 6
 ccaccagua gaagcgucuc cuuuggggua aucugaacag gugccgaccc agauggccac 6
 0
 gucuaccagu ccagcaccaa ucccuucaca gaguccuucc acggaggaag uacgaugaau 12
 0
 auuaauaguu gaauuuuacu cagggcuucc uugguccaga uagaugauag cuucaauggg 18
 0
 aagagguccu gaacauucag cuccauuaaa gguaaaauac cagcguugac agcaagcauu 24
 0
 ccugcauuug agccgaagcg agccacugaa cagaacucga agagcgugu uggaucgcau 30
 0
 cuuugugaau guacauuccg caauuuuccc aagaucuaug ccauaauuaa gugaacucca 36
 0
 ugaacacugc uuguaguug ggguccagga uuccucaaag cuu 40
 3

<210> 7
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:carboxy-terminal amino acids of REMODELIN

<400> 7

Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu Leu Pro Lys
 1 5 10 15

<210> 8

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:insulin signal peptide

<400> 8

Met Ala Leu Leu Val His Phe Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15

Trp Glu Pro Lys Pro Thr Gln Ala
 20

<210> 9

<211> 734

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:myc-tagged REMODELIN construct

<400> 9

atggccccca aggcgcgcgc gcctccccac agctgctgct cggcctcttc cttgtgctac 6
 0
 tgctgcttct gcagctgtcc gcgcgcgtcca gcgcctctga gaatcccaag gtgaagcaaa 12
 0
 aagcgtgat ccggcagagg gaagtggtag acctgtataa tgggatgtgc ctacaaggac 18
 0
 cagcaggagt tcctggctgc gatgggagcc ctggggccaa tggcattcct ggcacaccgg 24
 0
 gaatcccagg tcgggatgga ttcaaaggag agaaagggga gtgcttaagg gaaagctttg 30
 0
 aggaatcctg gacccccaaac tacaagcagt gttcatggag ttcacttaat tatggcatag 36
 0
 atcttgggaa aattgcggaa tgtacattca caaagatgcg atccaacagc gctcttcgag 42
 0
 ttctgttcag tggctcgctt cggctcaa atgcaggaatgc ttgctgtcaa cgctgggtatt 48
 0
 ttacctttaa tggagctgaa tgttcaggac ctcttcccat tgaagctatc atctatctgg 54

0
accaaggaag ccctgagtta aattcaacta ttaatatcca tcgtacttcc tccgtggaag 60
0
gactctgtga agggattggt gctggactgg tagacgtggc catctgggtc ggcacctgtt 66
0
cagattaccc caaaggagac gcttctactg ggtggaattc tgtgtcccgc atcatcattg 72
0
aagaactacc aaaa 73
4

10045992-104904